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Species tree, frequent HGT and gene conversions in Bdelloid Rotifers

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Abstract: The vast majority of animals reproduce sexually, i.e. with recombination of genetic material between generations. This genetic mixing is thought to favor the persistence of sexual lineages despite a theoretical advantage of asexuals regarding colonization capacity and population growth. In this context Bdelloid Rotifers, a highly diversified group of animals evolving asexually for millions of years, appears as a puzzle but also as an outstanding model to better understand long-term evolution in the absence of sexual reproduction.

The sequencing of the first Bdelloid Rotifer genome (Flot et al. 2013) revealed a peculiar organization, characterized by a degenerate tetraploidy, numerous rearrangements and the absence of homologous chromosomes. This structure, incompatible with meiosis, likely testifies the long asexual evolution of this genome. Besides, population genetic studies suggest that Bdelloids might exchange DNA within and between species, which likely plays a major role in their evolutionary history (Debortoli et al. 2016).

To better understand the dynamics of gene conversion and horizontal genetic transfers on these asexually evolving genomes and their importance in the success of Bdelloids, we are generating genomic data (RAD sequencing) from a large number of species distributed across the four existing families. We will show how methods involving the reconciliation of gene and species trees can help resolving species phylogeny of Bdelloids despite asexuality, polyploidy, gene conversions, transfers and losses. The resolution of the species tree is indeed a requirement for further study of the dynamics of horizontal transfers, which might play a key role in their evolution.

Expanded summary*: The vast majority of animals reproduce sexually, i.e. with recombination of genetic material between generations. This is despite a theoretical advantage of asexuals regarding colonization capacity and population growth and thus, it prompted the hypothesis that recombination of polymorphic loci allowed by sexual reproduction might favor the persistence of sexual lineages. In this context Bdelloid Rotifers, a highly diversified group of animals evolving asexually for millions of years, appears as a puzzle but also as an outstanding model to better understand long-term evolution in the absence of sexual reproduction.

The sequencing of the first Bdelloid Rotifer genome (Flot *et al.* 2013) revealed a peculiar organization, characterized by a degenerate tetraploidy, numerous rearrangements and the absence of homologous chromosomes. This structure, incompatible with meiosis, likely testifies the long asexual evolution of this genome. Besides, population genetic studies suggest that Bdelloids might exchange DNA within and between species, which likely plays a major role in their evolutionary history (Debortoli *et al.* 2016).

Our project aims at a better understanding of the importance of these genetic transfers in the success of Bdelloids. We are generating genomic data (RAD sequencing) from a large number of species sampled in the wild and distributed across the four existing families. This data will be useful to investigate the genomic history and dynamic of Bdelloids genomes. However, clonal lineages and partial polyploidy, associated with a significant rate of gene conversions and potential horizontal transfers might hinder the resolution of species phylogeny. We will show how methods involving the reconciliation of gene and species trees can help resolving the species phylogeny of Bdelloids despite asexuality, polyploidy, gene conversions, transfers and losses.

The resolution of the species tree is indeed a requirement for further study of the dynamics of horizontal transfers, which might play a key role in Bdelloid evolution. It will allow quantifying recombination between lineages, at different time scale, and thus provide insights on the genomic and ecological determinant of these transfers. Do gene transfers mainly occurs within closely related genetic clusters or also on a larger scale as is suggested by the high percentage of horizontally acquired genes non-metazoan origin in *Adineta vaga*'s genomes? Another striking characteristic of Bdelloids is their ability to withstand desiccation at any life stages. Such desiccation events have been shown to result in numerous double strand breaks in genomes, which are subsequently repaired (Hespeels *et al.* 2014). This observation led to the hypothesis that these events might favor the integration of foreign DNA in Bdelloid genomes. Thus, a better understanding of the dynamic and evolutionary importance of horizontal transfers between Bdelloid's

genomes will be complementary to studies allowing a direct measure of the impact of desiccations on horizontal transfers between rotifers.

Keywords:
Bdelloid rotifers, sex evolution, phylogenetics

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